Appendix B

NetPhos 2.0 Server - prediction results

Technical University of Denmark

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  454 Drosophila
MDYDFKMKTQIERTKVEDLFNYEGCKVGRGTYGHVYKAKWKETSDGKEYALKQIDGTGLSMSACREIALLRELKHQNVIT
LIRVFLSHNDRKVFLLIDYAEHDLWHIIKFHRAAKATKKQVVVPRGMVKSLLYQILDGIHYLHSNWVLHRDLKPANILVM
GDGNERGRVKIADMGFARLFNAPLKPLADLDPVVVTFWYRAPELLLGARHYTKAIDIWAIGCIFAELLTSEPIFHCRQED
IKTSNPYHHDQLDRIFNVMGFPQDKDWEDIKKMPEHHTLTKDFKRSTYSTCSLAKYMERHKIKPDSKAFHLLQKLLLMDP
NKRITSEQAMQDQYFQEEPQPTQDVFAGCPIPYPKREFLTDDDQEDKSDNKRQQQQQQQQQQQQQQQQQQQQQQQQQQQ
MNAEPNAKRVRLSGAGNQQDFHHQQQQQQQQQQQQQQQQQMMFNQQQNFQRFN
.............T.................T...........TS.................S.................
......S.....................................T.....................................
.....................................................................................
.....................................................S..S..............S.............
....T.................T.....................................................
............S.....................................
```

Phosphorylation sites predicted: Ser: 7 Thr: 6 Tyr: 0

Serine predictions

Name	Pos	Context v	Score	Pred
Drosophila	44	WKETSDGKE	0.612	*S*
Drosophila	60	GTGLSMSAC	0.213	.
Drosophila	62	GLSMSACRE	0.803	*S*
Drosophila	87	RVFLSHNDR	0.936	*S*
Drosophila	130	GMVKSLLYQ	0.009	.
Drosophila	144	HYLHSNWVL	0.003	.
Drosophila	230	ELLTSEPIF	0.010	.
Drosophila	244	DIKTSNPYH	0.021	.
Drosophila	286	DFKRSTYST	0.986	*S*
Drosophila	289	RSTYSTCSL	0.648	*S*
Drosophila	292	YSTCSLAKY	0.020	.
Drosophila	306	IKPDSKAFH	0.902	*S*
Drosophila	326	KRITSEQAM	0.259	.
Drosophila	368	QEDKSDNKR	0.454	.
Drosophila	413	RVRLSGAGN	0.970	*S*

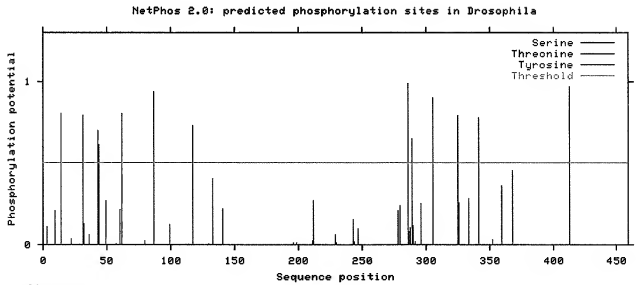
Threonine predictions

Name	Pos	Context v	Score	Pred
Drosophila	9	FKMKTQIER	0.211	.
Drosophila	14	QIERTKVED	0.806	*T*
Drosophila	31	VGRGTYGHV	0.788	*T*
Drosophila	43	KWKETSDGK	0.698	*T*
Drosophila	57	QIDGTGLSM	0.008	.
Drosophila	80	QNVITLIRV	0.025	.
Drosophila	117	AAKATKKQV	0.729	*T*

Drosophila	196	PVVVTFWYR	0.012	.
Drosophila	212	ARHYTKAID	0.271	.
Drosophila	229	AELLTSEPI	0.063	.
Drosophila	243	EDIKTSNPY	0.156	.
Drosophila	278	PEHHTLTKD	0.211	.
Drosophila	280	HHTLTKDFK	0.238	.
Drosophila	287	FKRSTYSTC	0.077	.
Drosophila	290	STYSTCSLA	0.116	.
Drosophila	325	NKRITSEQA	0.791	*T*
Drosophila	342	EPQPTQDVF	0.779	*T*
Drosophila	360	REFLTDDDQ	0.361	.

Tyrosine predictions

Name	Pos	Context	Score	Pred
Drosophila	3	--MDYDFKM	0.108	.
Drosophila	22	DLFNYEGCK	0.039	.
Drosophila	32	GRGTYGHVY	0.127	.
Drosophila	36	YGHVYKAKW	0.061	.
Drosophila	49	DGKEYALKQ	0.270	.
Drosophila	99	LLIDYAEHD	0.123	.
Drosophila	133	KSLLYQILD	0.404	.
Drosophila	141	DGIHYLHSN	0.221	.
Drosophila	199	VTFWYRAPE	0.012	.
Drosophila	211	GARHYTKAI	0.022	.
Drosophila	247	TSNPYHHDQ	0.099	.
Drosophila	288	KRSTYSTCS	0.105	.
Drosophila	296	SLAKYMERH	0.249	.
Drosophila	334	MQDQYFQEE	0.281	.
Drosophila	353	CPIPYPKRE	0.031	.



464 Human
MDYDFKVKLSSERERVEDLFEYEGCKVGRGTYGHVYKAKRKDGKDDKDYALKQIEGTGISMSACREIALLRELKHPNVIS
LQKVFLSHADRKVWLLFDYAEHDLWHIIKFHRASKANKKPVQLPRGMVKSLLYQILDGIHYLHANWVLHRDLKPANILVM
GEGPERGRVKIADMGFARLFNSPLKPLADLDPVVVTFWYRAPELLLGARHYTKAIDIWAIGCIFAELLTSEPIFHCRQED

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IKTSNPYHHDQLDRIFNVMGFPADKDWEDIKKMPEHSTLMKDFRRNTYTNCSLIKYMEKHKVKPDSKAFHLLQKLLTMDP
IKRITSEQAMQDPYFLEDPLPTSDVFAGCQIPYPKREFLTEEEPDDKGDKKNQQQQQGNNHTNGTGHPGNQDSSHTQGPP
LKKVRVVPPTTTSGGLIMTSDYQRSNPHAAYPNPGPSTSQPQSSMGYSATSQQPPQYSHQTHRY
.........SS.....................T.................Y............S..................
......S.........................S.....................................................
.....................................................................................
.....................................ST........TY.................S.............
....TS..............T.................T.....................................S......
..........TT.........Y.......Y.....S.....SS......S.........T...
```

Phosphorylation sites predicted: Ser: 13 Thr: 9 Tyr: 4

Serine predictions

Name	Pos	Context	Score	Pred
		v		
Human	10	KVKLSSERE	0.996	*S*
Human	11	VKLSSERER	0.996	*S*
Human	60	GTGISMSAC	0.058	.
Human	62	GISMSACRE	0.719	*S*
Human	80	PNVISLQKV	0.002	.
Human	87	KVFLSHADR	0.773	*S*
Human	114	FHRASKANK	0.955	*S*
Human	130	GMVKSLLYQ	0.009	.
Human	182	RLFNSPLKP	0.050	.
Human	230	ELLTSEPIF	0.010	.
Human	244	DIKTSNPYH	0.021	.
Human	277	MPEHSTLMK	0.596	*S*
Human	292	YTNCSLIKY	0.033	.
Human	306	VKPDSKAFH	0.938	*S*
Human	326	KRITSEQAM	0.813	*S*
Human	343	PLPTSDVFA	0.251	.
Human	393	GNQDSSHTQ	0.048	.
Human	394	NQDSSHTQG	0.963	*S*
Human	413	PTTTSGGLI	0.016	.
Human	420	LIMTSDYQR	0.029	.
Human	425	DYQRSNPHA	0.010	.
Human	437	NPGPSTSQP	0.626	*S*
Human	439	GPSTSQPQS	0.268	.
Human	443	SQPQSSMGY	0.789	*S*
Human	444	QPQSSMGYS	0.880	*S*
Human	448	SMGYSATSQ	0.095	.
Human	451	YSATSQQPP	0.643	*S*
Human	458	PPQYSHQTH	0.029	.
		^		

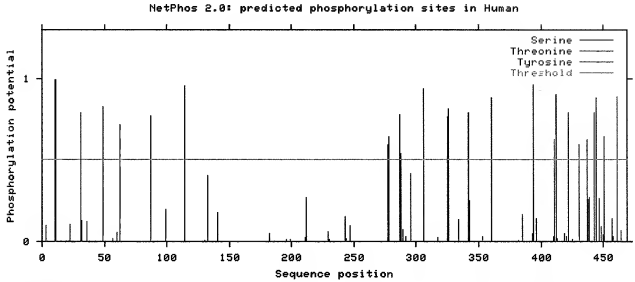
Threonine predictions

Name	Pos	Context	Score	Pred
		v		
Human	31	VGRGTYGHV	0.788	*T*
Human	57	QIEGTGISM	0.021	.
Human	196	PVVVTFWYR	0.012	.
Human	212	ARHYTKAID	0.271	.
Human	229	AELLTSEPI	0.063	.
Human	243	EDIKTSNPY	0.156	.
Human	278	PEHSTLMKD	0.645	*T*
Human	287	FRRNTYTNC	0.777	*T*
Human	289	RNTYTNCSL	0.076	.

Human	317	QKLLTMDPI	0.024	.
Human	325	IKRITSEQA	0.769	*T*
Human	342	DPLPTSDVF	0.794	*T*
Human	360	REFLTEEEP	0.885	*T*
Human	382	GNNHTNGTG	0.004	.
Human	385	HTNGTGHPG	0.167	.
Human	396	DSSHTQGPP	0.141	.
Human	410	VVPPTTTSG	0.033	.
Human	411	VPPTTTSGG	0.628	*T*
Human	412	PPTTTSGGL	0.901	*T*
Human	419	GLIMTSDYQ	0.047	.
Human	438	PGPSTSQPQ	0.256	.
Human	450	GYSATSQQP	0.040	.
Human	461	YSHQTHRY-	0.887	*T*

Tyrosine predictions

Name	Pos	Context	Score	Pred
Human	3	--MDYDFKV	0.100	.
Human	22	DLFEYEGCK	0.106	.
Human	32	GRGTYGHVY	0.127	.
Human	36	YGHVYKAKR	0.121	.
Human	49	DDKDYALKQ	0.827	*Y*
Human	99	LLFDYAEHD	0.199	.
Human	133	KSLLYQILD	0.404	.
Human	141	DGIHYLHAN	0.179	.
Human	199	VTFWYRAPE	0.012	.
Human	211	GARHYTKAI	0.022	.
Human	247	TSNPYHHDQ	0.099	.
Human	288	RRNTYTNCS	0.539	*Y*
Human	296	SLIKYMEKH	0.417	.
Human	334	MQDPYFLED	0.137	.
Human	353	CQIPYPKRE	0.033	.
Human	422	MTSDYQRSN	0.788	*Y*
Human	431	PHAAYPNPG	0.596	*Y*
Human	447	SSMGYSATS	0.262	.
Human	457	QPPQYSHQT	0.140	.
Human	464	QTHRY----	0.066	.



205 Mouse

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MYFTDKDWEDIKKMPEHSTLMKDFRRNTYTNCSLIKYMEKHKVKPDSKAFHLLQKLLTMDPIKRITSEQAMQDPYFLEDP
LPTSDVFAGCQIPYPKREFLTEEEPDEKGDKKTQQQQQGNNHTNGTGHPGNQDSGHAQGPPLKKVRVVPPTTTSGGLIMT
SDYQRSNPHAAYPNPGPSTSQPQSSMGYSATSQQPPQYSHQTHRY
...T.............ST.......TY.................S.................TS.............
..T.................T.................................................TT.......
..Y........Y.....S.....SS......S.........T...
```

Phosphorylation sites predicted: Ser: 7 Thr: 9 Tyr: 3

Serine predictions

Name	Pos	Context v	Score	Pred
Mouse	18	MPEHSTLMK	0.596	*S*
Mouse	33	YTNCSLIKY	0.033	.
Mouse	47	VKPDSKAFH	0.938	*S*
Mouse	67	KRITSEQAM	0.813	*S*
Mouse	84	PLPTSDVFA	0.251	.
Mouse	134	GNQDSGHAQ	0.198	.
Mouse	154	PTTTSGGLI	0.016	.
Mouse	161	LIMTSDYQR	0.029	.
Mouse	166	DYQRSNPHA	0.010	.
Mouse	178	NPGPSTSQP	0.626	*S*
Mouse	180	GPSTSQPQS	0.268	.
Mouse	184	SQPQSSMGY	0.789	*S*
Mouse	185	QPQSSMGYS	0.880	*S*
Mouse	189	SMGYSATSQ	0.095	.
Mouse	192	YSATSQQPP	0.643	*S*
Mouse	199	PPQYSHQTH	0.029	.

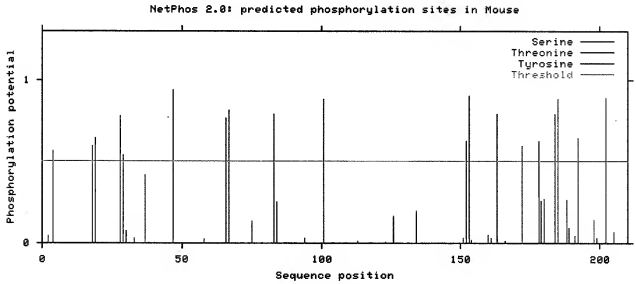
Threonine predictions

Name	Pos	Context v	Score	Pred
Mouse	4	-MYFTDKDW	0.567	*T*
Mouse	19	PEHSTLMKD	0.645	*T*
Mouse	28	FRRNTYTNC	0.777	*T*
Mouse	30	RNTYTNCSL	0.076	.

Mouse	58	QKLLTMDPI	0.024	.
Mouse	66	IKRITSEQA	0.769	*T*
Mouse	83	DPLPTSDVF	0.794	*T*
Mouse	101	REFLTEEEP	0.885	*T*
Mouse	113	GDKKTQQQQ	0.015	.
Mouse	123	GNNHTNGTG	0.004	.
Mouse	126	HTNGTGHPG	0.167	.
Mouse	151	VVPPTTTSG	0.033	.
Mouse	152	VPPTTTSGG	0.628	*T*
Mouse	153	PPTTTSGGL	0.901	*T*
Mouse	160	GLIMTSDYQ	0.047	.
Mouse	179	PGPSTSQPQ	0.256	.
Mouse	191	GYSATSQQP	0.040	.
Mouse	202	YSHQTHRY-	0.887	*T*

Tyrosine predictions

Name	Pos	Context	Score	Pred
Mouse	2	---MYFTDK	0.043	.
Mouse	29	RRNTYTNCS	0.539	*Y*
Mouse	37	SLIKYMEKH	0.417	.
Mouse	75	MQDPYFLED	0.137	.
Mouse	94	CQIPYPKRE	0.033	.
Mouse	163	MTSDYQRSN	0.788	*Y*
Mouse	172	PHAAYPNPG	0.596	*Y*
Mouse	188	SSMGYSATS	0.262	.
Mouse	198	QPPQYSHQT	0.140	.
Mouse	205	QTHRY----	0.066	.



Explain the output. Go back.